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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 04:25:46 : Search time 93 Seconds
(without alignments)
420.956 Million cell updates/sec

Title: us-09-895-298a-83

Perfect score: 1002

Sequence: 1 MMNFQPSKAMRASQMTFF.....HDSLDLRSSRVSQGNPRA 190

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|--------|----|--------|--------------------|
| 1 | 1002 | 100.0 | 330 | 4 | Q9H8I7 | Q9H8I7 homo sapien |
| 2 | 857 | 85.5 | 757 | 11 | Q9D4F1 | Q9D4F1 mus musculu |
| 3 | 292.5 | 29.2 | 444 | 4 | Q43284 | Q43284 homo sapien |
| 4 | 292.5 | 29.2 | 811 | 4 | Q8RE07 | Q8RE07 homo sapien |
| 5 | 287.5 | 28.7 | 450 | 11 | Q99J32 | Q99J32 mus musculu |
| 6 | 186.5 | 18.6 | 373 | 11 | Q99K19 | Q99K19 mus musculu |
| 7 | 118 | 11.8 | 402 | 4 | Q9H766 | Q9H766 homo sapien |
| 8 | 107.5 | 10.7 | 1247 | 5 | Q966F8 | Q966F8 caenorhabdi |
| 9 | 99.5 | 9.9 | 888 | 11 | Q8R4P4 | Q8R4P4 mus musculu |
| 10 | 97.5 | 9.7 | 282 | 11 | Q8R1X9 | Q8R1X9 mus musculu |
| 11 | 97 | 9.7 | 214 | 4 | Q9HYN5 | Q9HYN5 homo sapien |
| 12 | 97 | 9.7 | 890 | 4 | Q8RD17 | Q8RD17 homo sapien |
| 13 | 94.5 | 9.4 | 451 | 16 | Q97MNO | Q97MNO clostridium |
| 14 | 91.5 | 9.1 | 757 | 11 | Q9D435 | Q9D435 mus musculu |
| 15 | 91.5 | 9.1 | 757 | 11 | Q8R4P5 | Q8R4P5 mus musculu |
| 16 | 90.5 | 9.0 | 760 | 4 | Q8TD18 | Q8TD18 homo sapien |

| | | | | | | |
|----|------|-----|-----|----|--------|--------------------|
| 17 | 88.5 | 8.8 | 706 | 4 | Q8TB57 | Q8TB57 homo sapien |
| 18 | 88 | 8.8 | 322 | 16 | Q07420 | Q07420 mycobacteri |
| 19 | 87.5 | 8.7 | 261 | 5 | Q18875 | Q18875 caenorhabdi |
| 20 | 87 | 8.7 | 272 | 10 | Q9MOB7 | Q9MOB7 arabidopsis |
| 21 | 86.5 | 8.6 | 365 | 17 | Q8TM73 | Q8TM73 methanosarc |
| 22 | 84.5 | 8.4 | 713 | 16 | Q9KG35 | Q9KG35 bacillus ha |
| 23 | 84 | 8.4 | 148 | 10 | Q8S8M8 | Q8S8M8 arabidopsis |
| 24 | 84 | 8.4 | 273 | 10 | Q8S8O6 | Q8S8O6 arabidopsis |
| 25 | 81.5 | 8.1 | 154 | 16 | Q92AC4 | Q92AC4 listeria in |
| 26 | 81.5 | 8.1 | 261 | 16 | Q8T0C8 | Q8T0C8 anabaena sp |
| 27 | 81 | 8.1 | 204 | 9 | Q8SBD6 | Q8SBD6 staphylococ |
| 28 | 80.5 | 8.0 | 200 | 16 | Q9KCU0 | Q9KCU0 bacillus ha |
| 29 | 80.5 | 8.0 | 267 | 17 | Q9HUJ3 | Q9HUJ3 thermoplasm |
| 30 | 80 | 8.0 | 303 | 16 | Q99ZE3 | Q99ZE3 streptococc |
| 31 | 80 | 8.0 | 378 | 3 | Q12006 | Q12006 saccharomyc |
| 32 | 80 | 8.0 | 443 | 8 | Q33550 | Q33550 leishmania |
| 33 | 79.5 | 7.9 | 154 | 16 | Q8Y656 | Q8Y656 listeria mo |
| 34 | 79.5 | 7.9 | 217 | 16 | Q8ZSC1 | Q8ZSC1 anabaena sp |
| 35 | 79.5 | 7.9 | 396 | 16 | Q99V76 | Q99V76 staphylococ |
| 36 | 79.5 | 7.9 | 476 | 5 | Q8T1Y3 | Q8T1Y3 dictyosteli |
| 37 | 79.5 | 7.9 | 589 | 16 | Q912K4 | Q912K4 streptomyce |
| 38 | 79.5 | 7.9 | 704 | 5 | Q8T1P6 | Q8T1P6 dictyosteli |
| 39 | 79.5 | 7.9 | 772 | 16 | Q97LD1 | Q97LD1 clostridium |
| 40 | 79.5 | 7.9 | 913 | 5 | Q97272 | Q97272 plasmodium |
| 41 | 79 | 7.9 | 218 | 5 | Q9N895 | Q9N895 plasmodium |
| 42 | 79 | 7.9 | 239 | 16 | Q8Z8B7 | Q8Z8B7 salmonella |
| 43 | 78.5 | 7.8 | 229 | 16 | Q99KX0 | Q99KX0 staphylococ |
| 44 | 78 | 7.8 | 319 | 5 | Q9XV63 | Q9XV63 caenorhabdi |
| 45 | 78 | 7.8 | 552 | 5 | Q950K9 | Q950K9 caenorhabdi |

ALIGNMENTS

RESULT 1

ID Q9H8I7 PRELIMINARY: PRT: 330 AA.
AC Q9H8I7:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CDNA FLJ13593 fls, clone PLACE1009493.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishi S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.,
RT "NEO human cDNA sequencing project."
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK021655; BAB14629.1; -
SQ SEQUENCE 330 AA; 38958 MW; EBA21A1AC1455C2E CRC64;

Query Match 100.0%; Score 1002; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 3.8e-87;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | |
|----|-----|--|
| QY | 1 | MMNFQPSKAMRASQMTFFILFPSTGVLCITAITIMRLKPSADCGPRGLPLFIH 60 |
| DB | 141 | MMNFQPSKAMRASQMTFFILFPSTGVLCITAITIMRLKPSADCGPRGLPLFIH 200 |
| QY | 61 | SIYSWIDTSTRPGYLVVWVIRNLIGSVHFFILFLVILVILVYVWQTEGRKIMIRLL 120 |
| DB | 201 | SIYSWIDTSTRPGYLVVWVIRNLIGSVHFFILFLVILVILVYVWQTEGRKIMIRLL 260 |

OY 121 HEQIINEGDKMFLIEKLIKLOMEKANSSVLEREEQGGFLHGHGSDSLDRS 180
 DB 261 HEQIINEGDKMFLIEKLIKLOMEKANSSVLEREEQGGFLHGHGSDSLDRS 320
 OY 181 RSVOEGNPRA 190
 DB 321 RSVOEGNPRA 330

RESULT 2

O9DAFL PRELIMINARY: PRT: 757 AA.
 AC O9DAFL;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE 4932443108RIK protein.
 GN 4932443108RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shidata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glassi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Stambli F., Suzuki R., Tomita M., Wagner I., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
 RA Blake J., Boffelli D., Bojunga N., Carrincci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shidata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK016573; BAB30314.1; -;
 DR MGI:1921674; 4932443108RIK
 SQ SEQUENCE 757 AA; 87667 MW; 320D61A71CF5DAE CRC64;

Query Match 85.5%; Score 857; DB 11; Length 757;
 Best Local Similarity 87.4%; Pred. No. 5, 1e-73;
 Matches 166; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

OY 1 MANNPPSKAMRASOMTFIFLFFPSPGVCTLAITIMRLKPSADCGPFGGLPLFIH 60
 DB 568 MANNPPSKAMRASOMTFIFLFFPSPGVCTLAITIMRLKPSADCGPFGGLPSFIQ 627
 OY 61 STYSWIDTSTRPGYLWVWYVYRNIGSVHFFILITLIVITLYWQITTEGRKIMRL 120
 DB 628 STYSWIDTSTRPGYLWVWYVYRNIGSVHFFILITLIVITLYWQITTEGRKIMRL 687
 OY 121 HEQIINEGDKMFLIEKLIKLOMEKANSSVLEREEQGGFLHGHGSDSLDRS 180
 DB 688 HEQIINEGDKMFLIEKLIKLOMEKANSSVLEREEQGGFLHGHGSDSLDRS 747
 OY 181 RSVOEGNPRA 190
 DB 748 RSVOEGNPRA 757

RESULT 3

O43284

ID O43284 PRELIMINARY: PRT: 444 AA.
 AC O43284;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE LAK-4p (Expressed in activated T/LAK lymphocytes).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPHOID;
 RA Abe Y., Takaoka Y.;
 RT "LAK-4 clone from the membrane lymphotoxin expressing subtraction
 library";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB002405; BAA24179.2; -;
 DR EMBL: BC018346; AAH18346.1; -;
 DR InterPro: IPR000515; BPD_transp.
 DR PROSITE: PS00402; BPD_TRANSF_INN_MDMR; UNKNOWN.1.
 SQ SEQUENCE 444 AA; 50427 MW; DD4053A374A00FA1 CRC64;

Query Match 29.2%; Score 292.5; DB 4; Length 444;
 Best Local Similarity 34.9%; Pred. No. 1, 1e-19;
 Matches 60; Conservative 36; Mismatches 63; Indels 13; Gaps 2;

OY 1 MANNPPSKAMRASOMTFIFLFFPSPGVCTLAITIMRLKPSADCGPFGGLPLFIH 60
 DB 272 LANCQAPRRWLAHSHSTVLTLCPPAFGAFLCYANWQKPSCTGCPFFLDTMYE 331
 OY 61 STYSWIDTSTRPGYLWVWYVYRNIGSVHFFILITLIVITLYWQITTEGRKIMRL 119
 DB 332 AGRWVYHNLAAAPRVSMLPWHRYLMENTFFELVSALLAVYINIGVRCQKVICL 391
 OY 120 LHEQIINEGDKMFLIEKLIKLOD-----MEKANSSVLERE 159
 DB 392 LKEQISNEGDKFLINKLHSYERERERSRVGTTEAAPPALTTDQD 443

RESULT 4

O8TEQ7 PRELIMINARY: PRT: 811 AA.
 AC O8TEQ7;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE FLJ00136 protein (Fragment).
 GN FLJ00136.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
 RT "The nucleotide sequence of a long cDNA clone isolated from human
 spleen";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK074065; BAB84891.1; -;
 FT NON_TER 1
 SQ SEQUENCE 811 AA; 90727 MW; 346FE61A2C44B23 CRC64;

Query Match 29.2%; Score 292.5; DB 4; Length 811;
 Best Local Similarity 34.9%; Pred. No. 2e-19;
 Matches 60; Conservative 36; Mismatches 63; Indels 13; Gaps 2;

```

OY 1 MANNPQPSKAMWASOMTFEFLFFEPSTGYLCPLATITWMLKPSADCGPRRGDLPFIH 60
DB 639 IANCAAPRRPWLAHSMSTVFLLTLCFPAFLGAAYFLCYAWWQVKSSTCGPRTIDTMYE 698
OY 61 SIYSWIDTL-STRPGYLWWVWYIRMLIGSVHFFITITLITVLTLYLWQITGGRKIMRL 119
DB 699 AGRWVVRHLEAGRPVSNLPPVHRITMENTFFVFLVLSALLAVITLNTQVAVGQRKVICL 758
OY 120 LHEQIINEGKDKMFLIEKLIKIDMEKKRAN 159
DB 759 LKEQIINEGEDIKFLINKLSHYEKREPERSRVGTTEAANPALLTDEOD 810

RESULT 5
O99J32 PRELIMINARY; PRT; 450 AA.
O99J32
ID 099J32
AC 099J32
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Similar to expressed in activated T/LAK lymphocytes (Hypothetical 51.0
DE kDa protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004840; AAH04840.1; -
DR EMBL; BC013502; AAH13502.1; -
DR InterPro; IPR000515; BPD_transp.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; UNKNOWN_1.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 450 AA; 51009 MW; AF19129C11A53BD0 CRC64;

Query Match 28.7%; Score 287.5; DB 11; Length 450;
Best Local Similarity 37.7%; Pred. No. 3.3e-19;
Matches 57; Conservative 30; Mismatches 63; Indels 1; Gaps 1;

OY 1 MANNPQPSKAMWASOMTFEFLFFEPSTGYLCPLATITWMLKPSADCGPRRGDLPFIH 60
DB 272 MANNCAAPRRPWLAHSMSTVFLLTLCFPAFLGAAYFLCYAWWQVKSSTCGPRTINTMYE 331
OY 61 SIYSWIDTL-STRPGYLWWVWYIRMLIGSVHFFITITLITVLTLYLWQITGGRKIMRL 119
DB 332 AGTWVVRHLEAGRSASMSLPPMLHHLVENVTFLLFASALLAVITFNIDYVAVGQRKVICL 391
OY 120 LHEQIINEGKDKMFLIEKLIKIDMEKKRAN 150
DB 392 LKEQIINEGEDIKFLINKLSHYEEGRSRP 422

RESULT 6
O99K19 PRELIMINARY; PRT; 373 AA.
O99K19
ID 099K19
AC 099K19
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 42.3 kDa protein (Unknown) (Protein for MGC:12049).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP [1]

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RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC005510; AAH05510.1; -.
DR EMBL, BC006956; AAH06956.1; -.
DR InterPro; IPR000515; BPD_transp.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 373 AA; 13B4C5E8A0FB889 CRC64;

Query Match
Best Local Similarity 18.6%; Score 186.5; DB 11; Length 373;
Matches 36; Conservative 18; Mismatches 46; Indels 1; Gaps 1;

QY 1 MANNPPSKAMRASQMTFFILFFPPSTGYCLTATITMLKASDCGPPRGPLRPH 60
DB 272 MANNCAARRPRPMVASHSTFTLLCFPSFLGAAYFLCYAWQVRSSSTCGPRTINTWYE 331
QY 61 STYSWIDTLS-TRPGYLVWVYIRNLIGSVHFFITLITVL 100
DB 332 ACTWVVRLEHAGSGASHLPWLHPLHVLVENTFFFLASALLL 372

RESULT 7
O9H766 PRELIMINARY; PRT; 402 AA.
AC O9H766;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CDNA: FLJ12140 fis, clone COL01132.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoide; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Kawabata A., Hiki J T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isegai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL, AK024893; BAB15032.1; -.
SQ SEQUENCE 402 AA; 46254 MW; 716C11B5B794DC4 CRC64;

Query Match
Best Local Similarity 11.8%; Score 118; DB 4; Length 402;
Matches 40; Conservative 29; Mismatches 53; Indels 30; Gaps 5;

QY 5 QPPSKAMRASQMTFFILFFPPSTGYCLTATITWRIKPSADCGP-----R 53
DB 267 RSPSPFRFASNNFFELVLIGLCGLAT-PLTISIRIPSSKACGPFNTWTWEVLPK 325
QY 54 GRLPFIHSYVMDLSTRPGYLVWVYIRNLIGSVHFFITLITVLYTYXMDTEGR 113
DB 326 TVSTPSSSQSHIHGVTSE-----AFNVPPMIICTLM---FYIALAGAH 368
QY 114 KIMIRLHEQIINEGDKMFLLEKLIKQ-DM 144
DB 369 KRVTQLRQGLSLESRDKCYLQIKLTLEQRDM 400.

RESULT 8
O966F8 PRELIMINARY; PRT; 1247 AA.
AC O966F8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

```

DE Hypothetical protein T13G4.3.
 GN T13G4.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=9069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology, the C. elegans Sequencing Consortium.";
 RL Science 283:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Favellio T.;
 RT "The sequence of C. elegans cosmid T13G4.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC006685; AAR84572.1;
 SQ SEQUENCE 1247 AA; 142928 MW; F0B843BA38721E49 CRC64;

Query Match 10.7%; Score 107.5; DB 5; Length 1247;
 Best Local Similarity 26.5%; Pred. No. 0.11; Mismatches 29; Gaps 8;
 Matches 49; Conservative 32; Indels 29; Gaps 8;

QY 6 PPSKAMRASQMTFFFLFFPSTGVLCTLAIT-TIWRLPSPADCGPFGPLFTHSIY 63
 DB 736 PAEIRASASSNFYIGIL---TWLLCTLPYGFVIASMSPSRSCPF-----ARY 784
 QY 64 SWIDTSTRPGYLMV---VWIYRNIGSVHFFFLTLVLLITYLWQITEGRK-----I 115
 DB 785 QHFYTVTRIEKRVQDGTVALYRIHTASPGVPIILFLILLYFLFSLVRLGRLRENTDL 844
 QY 116 MIRLHEQIINECKDKMFLI-----EKLKLOMEKKANPSSLVLRREVEQGFHLGCE 170
 DB 845 QAOVLVHER--TEBKKEIFELAGKKNKFEKRD-KRKSNDYIPLIEQRREPRWROYHEME 901
 QY 171 HDGSL 175
 DB 902 ADHAL 906

RESULT 9
 Q8RAP4 PRELIMINARY; PRT; 888 AA.
 AC Q8RAP4;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Transmembrane cochlear-expressed protein 2.
 GN TMC2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21918583; PubMed=11850618;
 RA Kurima K., Peters L.M., Yang Y., Riazuddin S., Ahmed Z.M., Naz S.,
 Arnaud D., Drury S., Mo J., Makishima T., Ghosh M., Menon P.S.N.,
 Deshmukh D., Oddou C., Ostrer H., Khan S., Riazuddin S.,
 DeJonghe P.L., Hampton L.L., Sullivan S.L., Battey J.F.,
 Keats B.J.B., Wilcox E.R., Friedman T.B., Griffith A.J.;
 RT "Dominant and recessive deafness caused by mutations of a novel gene,
 TMC1, required for cochlear hair-cell function.";

RL Nat. Genet. 30:277-284(2002).
 DR EMBL; AF417581; AAL86402.1;
 SQ SEQUENCE 888 AA; 101134 MW; 6D834D7987768FA7 CRC64;
 Query Match 9.9%; Score 99.5; DB 11; Length 888;
 Best Local Similarity 21.5%; Pred. No. 0.46; Mismatches 72; Indels 81; Gaps 10;
 Matches 51; Conservative 33; Mismatches 72; Indels 81; Gaps 10;

QY 6 PPSKAMRASQMTFFFLFFPSTGVLCTLAITIRLKPSCADCGPFG-----54
 DB 663 PHERVEKASRNSNFYMGILLVFLSL--PVAYTVMSLPSPSCGPFSGKNRYDVLTHER 721
 QY 55 ----LPLFHSIYSWIDTLSTRPGYLMVWYIYNLIGSVHFFFLTLVLLITYLWQIT 110
 DB 722 IENDPFRFLCKIRAFPL---ANPG-----LIIPLALLMFLAIYIYNS 759
 QY 111 EGRKI-----MIRLHEQIIN---EGKDKMFLIEKLIK-----140
 DB 760 VSKSLRANAOQLKKIOALKEVEKNHKSITGKAIVYSEDTIRNSSKNATQIHLTKEPT 819
 QY 141 -----LODMEKKA-NPSSLVLRREVEQGFHLGHDGSLDRSRVQEGNPRA 190
 DB 820 SHSSQIQITLDRKKAQGPHTSTEGASPSISWHV---GSGPFRGR--DSGQPGS 870

RESULT 10
 Q8RLX9 PRELIMINARY; PRT; 282 AA.
 AC Q8RLX9;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Hypothetical 31.3 kDa protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary Gland;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022758; AAN22758.1;
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 282 AA; 31318 MW; 0E062EBED7645C7C CRC64;

Query Match 9.7%; Score 97.5; DB 11; Length 282;
 Best Local Similarity 28.3%; Pred. No. 0.22; Mismatches 49; Indels 35; Gaps 7;
 Matches 43; Conservative 25; Mismatches 49; Indels 35; Gaps 7;

QY 4 FOPSKAMRASQMTFFFLFFPSTGVLCTLAIT-----TIWRLPSPADCGPFGPL 56
 DB 145 YSPASRFRFRASTANFFPPVL-----LVGLAISVPVLYIFLIPSKLCGPFGRL 196
 QY 57 LPLFHSIYSWIDTL-STRPGYLMVWYIYNLIGSVHFFFLTLVLLITYLWQIT-----110
 DB 197 SIWAQLEAIESLPQTAQNPLX-----FLGQAF---TVPLLLISSTIMMYTVALAN 245
 QY 111 -EGKTIIRLHEQIINECKDKMFLIEKLIK 141
 DB 246 CYGR--LISELKROIETEVONKVFIAQRAVAL 275
 RESULT 11
 Q9BYN5 PRELIMINARY; PRT; 214 AA.
 AC Q9BYN5;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE DJ686C3.6 (Novel protein) (Fragment).
 GN DJ686C3.3.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL049712; CAC29096.1; -.
FT NON_TER 1
FT 214
SQ SEQUENCE 214 AA; 24357 MW; 079641A43CC112A7 CRC64;

Query Match
Best Local Similarity 24.8%; Score 97; DB 4; Length 214;
Matches 29; Conservative 18; Mismatches 32; Indels 38; Gaps 4;

QY 6 PPSKAMRASQMMTFEFLFPSTGVLCCTAATITWRKPSADGCPFG----- 54
DQ 100 PHERVFKASRNNFMYGLLLVFLSL-PVAYTIMSLPSPGDCGPGSKRMVDVLDQET 158
DB 159 IENDPFFLGKIFAF-----ANPG-----LIIPIALIMFLAIY 193

RESULT 12
08TD17 PRELIMINARY; PRT; 890 AA.
AC Q8TD17;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Transmembrane cochlear-expressed protein 2.
GN TMC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918583; PubMed=11850618;
RA Kurita K., Peters L.M., Yang Y., Riazuddin S., Ahmed Z.M., Naz S.,
RA Arnaud D., Druy S., Mo J., Makishima T., Ghosh M., Menon P.S.N.,
RA Deshmukh D., Oddoux C., Oestre H., Khan S., Riazuddin S.,
RA DeAngelis P.L., Hampton L.L., Sullivan S.L., Bailey J.F.,
RA Keats B.J.B., Wilcox E.R., Friedman T.B., Griffith A.J.;
RT "Dominant and recessive deafness caused by mutations of a novel gene,
RT TMC1, required for cochlear hair-cell function.";
RL Nat. Genet. 30:277-284(2002).
DR EMBL: AF417580; AAL86401.1; -.
SQ SEQUENCE 890 AA; 101006 MW; A35AE2216B2AC0C4 CRC64;

Query Match
Best Local Similarity 9.7%; Score 97; DB 4; Length 890;
Matches 29; Conservative 18; Mismatches 32; Indels 38; Gaps 4;

QY 6 PPSKAMRASQMMTFEFLFPSTGVLCCTAATITWRKPSADGCPFG----- 54
DQ 665 PHERVFKASRNNFMYGLLLVFLSL-PVAYTIMSLPSPGDCGPGSKRMVDVLDQET 723
DB 724 IENDPFFLGKIFAF-----ANPG-----LIIPIALIMFLAIY 758

RESULT 13
097MNO PRELIMINARY; PRT; 451 AA.
AC Q97MNO;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)

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DE Predicted ABC transporter, permease component.
GN CAC0165.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC SMPAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiti J., Wolf Y.I.,
RA Tatunov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007529; AAK78148.1; -.
KW Complete proteome.
SQ SEQUENCE 451 AA; 51856 MW; 5E48C4CA82842143 CRC64;

Query Match
Best Local Similarity 9.4%; Score 94.5; DB 16; Length 451;
Matches 35; Conservative 32; Mismatches 53; Indels 21; Gaps 6;

QY 23 LLEPSPFGVL-CCTAATITWRKPSADGCPFGDLPFIHSIYSWIDTLSTPGYIWMVI 81
DQ 104 LDFONAITETIGCALIGLIGML-----MFIISIMY-----TIMKTGGLIWMVN 149
DB 82 YRNIGSVHFFIITLIVLIITYLWQITGKRMIRLHEQIINEGDKMFL-TEKLIR 140
DQ 150 Y-SIGGTAIIFLQIVVYITIGDYSTR-----VIDLESKRSPREKRLSTAEITE 204
QY 141 LQMEKANPSSLVREKVE 161
DB 205 IIGMKKTSYKIKILINEDID 225

RESULT 14
09D435 PRELIMINARY; PRT; 279 AA.
AC Q9D435;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 4933416G09R1K protein.
GN 4933416G09R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudil F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Marzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;

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RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK016832; BAB30454.1; -
DR MGI:1921712; 4933416G09R1K.
SQ SEQUENCE 279 AA; 31965 MW; 71EAF324D407716E CRC64;

Query Match 9.1%; Score 91.5; DB 11; Length 279;
Best Local Similarity 20.7%; Pred. No. 0.81;
Matches 34; Conservative 27; Mismatches 58; Indels 45; Gaps 6;

QY 6 PPSKARASQMTFFFLFFPSFTGVLCATITIRLKPSADCGPFGILPLFI----- 59
DB 74 PEARVFKASRNNFYGLMLLIIFLSTMPYLIIV-SLPSPFCGPPSGKNRMEFYIGET 132
QY 60 --HSIYSWIDTL--STRPGYLWVWIYRNLIIGSVHFFFLTLVLIITYLWQIT-EGR 113
DB 133 LEHDFPSWMAKILRQLSNGLV-----IAVLVWVLIITYLIYNATAKG 175
QY 114 KIMIRLLHQIINEGKDKMFLIEKLIKIDMEKKANPSSIVLER 157
DB 176 KA-----ANLDLKKKKQQALENKMKRKKMAAR 204

RESULT 15

Q8R4P5 PRELIMINARY; PRT; 757 AA.
AC Q8R4P5;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Transmembrane cochlear-expressed protein 1.
GN TMC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21918583; PubMed-11850618;
RA Kurima K., Peters L.M., Yang Y., Riazuddin S., Ahmed Z.M., Naz S.,
RA Arnaud D., Drury S., Mo J., Makishima T., Ghosh M., Menon P.S.N.,
RA Deshmukh D., Oddoux C., Oster H., Khan S., Riazuddin S.,
RA Delinger P.L., Hampton L.L., Sullivan S.L., Batley J.F.,
RA Keats B.J.B., Wilcox E.R., Friedman T.B., Griffith A.D.,
RT "Dominant and recessive deafness caused by mutations of a novel gene,
RT TMC1, required for cochlear hair-cell function.";
RL Nat. Genet. 30:277-284(2002).
DR EMBL: AF417579; AAL86400.1; -
SQ SEQUENCE 757 AA; 87264 MW; 9FB6CB73A7DD367D CRC64;

Query Match 9.1%; Score 91.5; DB 11; Length 757;
Best Local Similarity 20.7%; Pred. No. 2.3;
Matches 34; Conservative 27; Mismatches 58; Indels 45; Gaps 6;

QY 6 PPSKARASQMTFFFLFFPSFTGVLCATITIRLKPSADCGPFGILPLFI----- 59
DB 619 PEARVFKASRNNFYGLMLLIIFLSTMPYLIIV-SLPSPFCGPPSGKNRMEFYIGET 677
QY 60 --HSIYSWIDTL--STRPGYLWVWIYRNLIIGSVHFFFLTLVLIITYLWQIT-EGR 113
DB 678 LEHDFPSWMAKILRQLSNGLV-----IAVLVWVLIITYLIYNATAKG 175
QY 114 KIMIRLLHQIINEGKDKMFLIEKLIKIDMEKKANPSSIVLER 157
DB 721 KA-----ANLDLKKKKQQALENKMKRKKMAAR 749

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